



RECEIVED

OCT 16 2002

SEQUENCE LISTING

TECH CENTER 1600/2900

(1) GENERAL INFORMATION:

(i) APPLICANT: Shuji Hinuma  
Yasuaki Ito  
Ryo Fujii

(ii) TITLE OF INVENTION: G Protein Coupled Receptor Protein,  
Production, And Use Thereof

(iii) NUMBER OF SEQUENCES: 61

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Edwards & Angell, LLP  
(B) P.O. Box 9169  
(C) CITY: BOSTON  
(D) STATE: MA  
(E) COUNTRY: USA  
(F) ZIP: 02209

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/461,436  
(B) FILING DATE: 14-DECEMBER-1999  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/513,974  
(B) FILING DATE: 14-SEP-1995

(A) APPLICATION NUMBER: PCT/JP95/01599  
(B) FILING DATE: 10-AUG-1995

(A) APPLICATION NUMBER: 7-093989  
(B) FILING DATE: 19-APR-1995

(A) APPLICATION NUMBER: 7-057186  
(B) FILING DATE: 16-MAR-1995

(A) APPLICATION NUMBER: 7-007177  
(B) FILING DATE: 20-JAN-1995

(A) APPLICATION NUMBER: 6-326611  
(B) FILING DATE: 28-DEC-1994

(A) APPLICATION NUMBER: 6-270017  
(B) FILING DATE: 02-NOV-1994

(A) APPLICATION NUMBER: 6-236357

(B) FILING DATE: 30-SEP-1994

(A) APPLICATION NUMBER: 6-236356

(B) FILING DATE: 30-SEP-1994

(A) APPLICATION NUMBER: 6-189274

(B) FILING DATE: 11-AUG-1994

(A) APPLICATION NUMBER: 6-189273

(B) FILING DATE: 11-AUG-1994

(A) APPLICATION NUMBER: 6-189272

(B) FILING DATE: 11-AUG-1994

(viii) ATTORNEY/AGENT INFORMATION

(A) NAME: CONLIN, DAVID G.

(B) REGISTRATION NUMBER 27,026

(C) REFERENCE/DOCKET NUMBER: 45753 DIV2

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 617-439-4444

(B) TELEFAX: 617-439-4170

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid  
Synthetic DNA

(iii) FEATURES: N is A, G, C, or T

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CGTGGSCMTS STGGGCAACN YCCTG 25

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid  
Synthetic DNA

(iii) FEATURES: N is A, G, C, or T

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GTNGWRRGGC ANCCAGCAGA KGGCAAA 27

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Other nucleic acid  
Synthetic DNA
- (iii) FEATURES: N is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CTCGCSGCMY TNRGYATGGA YCGNTAT 27

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Other nucleic acid  
Synthetic DNA
- (iii) FEATURES: N is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

CATGTRGWAG GGAANCCAGS AMANRARRAA 30

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Other nucleic acid  
Synthetic DNA
- (iii) FEATURES: N is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CTGACYGYTC TNRSNRYTGA CMGVTAC 27

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Other nucleic acid  
Synthetic DNA
- (iii) FEATURES: N is inosine
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

CTGACYGYTC TNRSNRYTGA CMGVTAT 27

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Other nucleic acid  
Synthetic DNA
- (iii) FEATURES: N is inosine
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CTCGCSGCMY TNRGYATGGA YCGNTAC 27

(2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Other nucleic acid  
Synthetic DNA
- (iii) FEATURES: N is inosine
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GATGTGRTAR GGSRNCCAAC AGANGRYAAA 30

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Other nucleic acid  
Synthetic DNA
- (iii) FEATURES: N is inosine
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GATGTGRTAR GGSRNCCAAC AGANGRYGAA 30

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Other nucleic acid  
Synthetic DNA
- (iii) FEATURES: N is inosine
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GYCACCAACN WSTTCATCCT SWNHCTG 27

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Other nucleic acid  
Synthetic DNA
- (iii) FEATURES: N is inosine
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

ASNSANRAAG SARTAGANGA NRGGRTT 27

(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Other nucleic acid  
Synthetic DNA
- (iii) FEATURES: N is inosine
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

TGNTSSTKMT NGSNGTKGTN GGNAA 25

(2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Other nucleic acid  
Synthetic DNA
- (iii) FEATURES: N is inosine
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

AYCKGTAYCK GTCCANKGWN ATKGC 25

(2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Other nucleic acid  
Synthetic DNA
- (iii) FEATURES: N is inosine
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

CATKKCCSTG GASAGNTAYN TRGC 24

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Other nucleic acid  
Synthetic DNA
- (iii) FEATURES: N is inosine
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GWWGGGSAKC CAGCASANGG CRAA 24

(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Other nucleic acid  
Synthetic DNA
- (iii) FEATURES: 15th N is A, G, C, or T  
6th, 9th, 10th & 12th Ns are inosine
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

ARYYTNGCNN TNGCNGAY 18

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Other nucleic acid  
Synthetic DNA
- (iii) FEATURES: 13th, 15th, 16th & 18th Ns are  
each A, G, C, or T  
1st, 4th, 6th Ns are inosine
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

NGGNANCCAR CANANNRNRA A 21

(2) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Other nucleic acid  
Synthetic DNA
- (iii) FEATURES: N is inosine
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

GCCTSNTNRN SATGWSTGTG GANMGNT 27

(2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Other nucleic acid  
Synthetic DNA
- (iii) FEATURES: N is inosine
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

GAWSNTGMYN ANRTGGWAGG GNANCCA 27

(2) INFORMATION FOR SEQ ID NO: 20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Other nucleic acid  
Synthetic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

TAGTGTGTGG AGTCGTGTGG CTGGCTG 27



(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid  
Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

AGTCTTTGCT GCCACAGGCA TCCAGCG 27

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid  
Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

CAAGCCAGTA AGGCTATGAA GGGCAGCAAG 30

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid  
Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

ACAGGACCTG CTGGGCCATC CTGGCGACAC A 31

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 91  
(B) TYPE: Amino acid  
(C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Leu Val Leu Val Ile Ala Arg Val Arg Arg Leu His Asn Val Thr Asn  
1 5 10 15  
Phe Leu Ile Gly Asn Leu Ala Leu Ser Asp Val Leu Met Cys Thr Ala  
20 25 30  
Cys Val Pro Leu Thr Leu Ala Tyr Ala Phe Glu Pro Arg Gly Trp Val  
35 40 45  
Phe Gly Gly Gly Leu Cys His Leu Val Phe Phe Leu Gln Pro Val Thr  
50 55 60  
Val Tyr Val Ser Val Phe Thr Leu Thr Thr Ile Ala Val Asp Arg Tyr  
65 70 75 80  
Val Val Leu Val His Pro Leu Arg Arg Arg Ile  
85 90

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59  
(B) TYPE: Amino acid  
(C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

Gly Leu Leu Leu Val Thr Tyr Leu Leu Pro Leu Leu Val Ile Leu Leu  
1 5 10 15  
Ser Tyr Val Arg Val Ser Val Lys Leu Arg Asn Arg Val Val Pro Gly  
20 25 30  
Cys Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg Arg Arg Arg  
35 40 45  
Thr Phe Cys Leu Leu Val Val Val Val Val  
50 55

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 370  
(B) TYPE: Amino acid  
(C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Met Ala Ser Ser Thr Thr Arg Gly Pro Arg Val Ser Asp Leu Phe Ser  
1 5 10 15  
Gly Leu Pro Pro Ala Val Thr Thr Pro Ala Asn Gln Ser Ala Glu Ala  
20 25 30  
Ser Ala Gly Asn Gly Ser Val Ala Gly Ala Asp Ala Pro Ala Val Thr  
35 40 45  
Pro Phe Gln Ser Leu Gln Leu Val His Gln Leu Lys Gly Leu Ile Val  
50 55 60  
Leu Leu Tyr Ser Val Val Val Val Val Gly Leu Val Gly Asn Cys Leu  
65 70 75 80  
Leu Val Leu Val Ile Ala Arg Val Arg Arg Leu His Asn Val Thr Asn  
85 90 95  
Phe Leu Ile Gly Asn Leu Ala Leu Ser Asp Val Leu Met Cys Thr Ala  
100 105 110  
Cys Val Pr

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Shuji Hinuma  
Masaki Hosoya  
Ryo Fujii  
Tetsuya Ohtaki  
Shoji Fukusumi

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Shuji Hinuma  
Masaki Hosoya  
Ryo Fujii  
Tetsuya Ohtaki  
Shoji Fukusumi

u Ala Ile Trp Ala Leu Ser Ala Val Leu Ala Leu  
180 185 190  
Pro Ala Ala Val His Thr Tyr His Val Glu Leu Lys Pro His Asp Val  
195 200 205  
Arg Leu Cys Glu Glu Phe Trp Gly Ser Gln Glu Arg Gln Arg Gln Leu  
210 215 220  
Tyr Ala Trp Gly Leu Leu Leu Val Thr Tyr Leu Leu Pro Leu Leu Val  
225 230 235 240  
Ile Leu Leu Ser Tyr Val Arg Val Ser Val Lys Leu Arg Asn Arg Val



Ala Tyr Ala Val Leu Ala Ile Trp Val Leu Ser Ala Val Leu Ala Leu  
100 105 110

Pro Ala Ala Val His Thr Tyr His Val Glu Leu Lys Pro His Asp Val  
115 120 125

Arg Leu Cys Glu Glu Phe Trp Gly Ser Gln Glu Arg Gln Arg Gln Leu  
130 135 140

Tyr Ala Trp Gly Leu Leu Leu Val Thr Tyr Leu Leu Pro Leu Leu Val  
145 150 155 160

Ile Leu Leu Ser Tyr Ala Arg Val Ser Val Lys Leu Arg Asn Arg Val  
165 170 175

Val Pro Gly Arg Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg  
180 185 190

Arg Arg Arg Thr Phe Cys Leu Leu Val Val Val Val Val Val  
195 200 205

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 126  
(B) TYPE: Amino acid  
(C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Val Val Leu Val His Pro Leu Arg Arg Arg Ile Ser Leu Arg Leu Ser  
1 5 10 15

Ala Tyr Ala Val Leu Gly Ile Trp Ala Leu Ser Ala Val Leu Ala Leu  
20 25 30

Pro Ala Ala Val His Thr Tyr His Val Glu Leu Lys Pro His Asp Val  
35 40 45

Ser Leu Cys Glu Glu Phe Trp Gly Ser Gln Glu Arg Gln Arg Gln Ile  
50 55 60

Tyr Ala Trp Gly Leu Leu Leu Gly Thr Tyr Leu Leu Pro Leu Leu Ala  
65 70 75 80

Ile Leu Leu Ser Tyr Val Arg Val Ser Val Lys Leu Arg Asn Arg Val  
85 90 95

Val Pro Gly Ser Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg  
100 105 110

Arg Arg Arg Thr Phe Cys Leu Leu Val Val Val Val Val Val  
115 120 125

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 273  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE  
(C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

```
CTGGTGCTGG TGATCGCGCG GGTGCGCCGG CTGCACAACG TGACGAACTT CCTCATCGGC   60
AACCTGGCCT TGTCCGACGT GTCATGTGC ACCGCCTGCG TGCCGCTCAC GCTGGCCTAT   120
GCCTTCGAGC CACGCGGCTG GGTGTTTCGGC GGCGGCCTGT GCCACCTGGT CTTCTTCCTG   180
CAGCCGGTCA CCGTCTATGT GTCGGTGTTT ACGCTCACCA CCATCGCAGT GGACCGGTAC   240
GTCGTGCTGG TGCACCCGCT GAGGCGGCGC ATC                               273
```

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 177  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE  
(C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

```
GGCCTGCTGC TGGTCACCTA CTGCTCCCT CTGCTGGTCA TCCTCCTGTC TTACGTCCGG   60
GTGTCAGTGA AGCTCCGCAA CCGCGTGGTG CCGGGCTGCG TGACCCAGAG CCAGGCCGAC   120
TGGGACCGCG CTCGGCGCCG GCGCACCTTC TGCTTGCTGG TGGTGGTCGT GGTGGTG   177
```

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1110

(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE

(C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

ATGGCCTCAT	CGACCACTCG	GGGCCCCAGG	GTTTCTGACT	TATTTTCTGG	GCTGCCGCCG	60
GCGGTCACAA	CTCCCGCCAA	CCAGAGCGCA	GAGGCCTCGG	CGGGCAACGG	GTCGGTGGCT	120
GGCGCGGACG	CTCCAGCCGT	CACGCCCTTC	CAGAGCCTGC	AGCTGGTGCA	TCAGCTGAAG	180
GGGCTGATCG	TGCTGCTCTA	CAGCGTCGTG	GTGGTCGTGG	GGCTGGTGGG	CAACTGCCTG	240
CTGGTGCTGG	TGATCGCGCG	GGTGCGCCGG	CTGCACAACG	TGACGAACTT	CCTCATCGGC	300
AACCTGGCCT	TGTCCGACGT	GTCATGTGTC	ACCGCCTGCG	TGCCGCTCAC	GCTGGCCTAT	360
GCCTTCGAGC	CACGCGGCTG	GGTGTTTCGGC	GGCGGCCTGT	GCCACCTGGT	CTTCTTCCTG	420
CAGCCGGTCA	CCGTCTATGT	GTCGGTGTTT	ACGCTCACCA	CCATCGCAGT	GGACCGCTAC	480
GTCGTGCTGG	TGCACCCGCT	GAGGCGGCGC	ATCTCGCTGC	GCCTCAGCGC	CTACGCTGTG	540
CTGGCCATCT	GGGCGCTGTC	CGCGGTGCTG	GCGCTGCCTG	CCGCCGTGCA	CACCTATCAC	600
GTGGAGCTCA	AGCCGCACGA	CGTGCGCCTC	TGCGAGGAGT	TCTGGGGCTC	CCAGGAGCGC	660
CAGCGCCAGC	TCTACGCCTG	GGGGCTGCTG	CTGGTCACCT	ACCTGCTCCC	TCTGCTGGTC	720
ATCCTCCTGT	CTTACGTCCG	GGTGTCAGTG	AAGTCCGCA	ACCGCGTGGT	GCCGGGCTGC	780
GTGACCCAGA	GCCAGGCCGA	CTGGGACCGC	GCTCGGCGCC	GGCGCACCTT	CTGCTTGCTG	840
GTGGTGGTCG	TGGTGGTGTT	CGCCGTCTGC	TGGCTGCCGC	TGCACGTCTT	CAACCTGCTG	900
CGGGACCTCG	ACCCCCACGC	CATCGACCCT	TACGCCTTTG	GGCTGGTGCA	GCTGCTCTGC	960
CACTGGCTCG	CCATGAGTTC	GGCCTGCTAC	AACCCCTTCA	TCTACGCCTG	GCTGCACGAC	1020
AGCTTCCGCG	AGGAGCTGCG	CAAACGTGTT	GTCGCTTGGC	CCCGCAAGAT	AGCCCCCAT	1080
GGCCAGAATA	TGACCGTCAG	CGTGGTCATC				1110

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 618  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE

(C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

```
CTGGTGCTGG TGATCGCGCG GGTGCGCCGG CTGTACAACG TGACGAATTT CCTCATCGGC 60
AACCTGGCCT TGTCCGACGT GCTCATGTGC ACCGCCTGCG TGCCGCTCAC GCTGGCCTAT 120
GCCTTCGAGC CACGCGGCTG GGTGTTTCGGC GCGGCGCTGT GCCACCTGGT CTTCTTCCTG 180
CAGGCGGTCA CCGTCTATGT GTCGGTGTTT ACGCTCACCA CCATCGCAGT GGACCGCTAC 240
GTCGTGCTGG TGCACCCGCT GAGGCGGCGC ATCTCGCTGC GCCTCAGCGC CTACGCTGTG 300
CTGGCCATCT GGGTGCTGTC CGCGGTGCTG GCGCTGCCCC CCGCCGTGCA CACCTATCAC 360
GTGGAGCTCA AGCCGCACGA CGTGCGCCTC TGCAGGAGT TCTGGGGCTC CCAGGAGCGC 420
CAGCGCCAGC TCTACGCTG GGGGCTGCTG CTGGTCACCT ACCTGCTCCC TCTGCTGGTC 480
ATCCTCCTGT CTTACGCCCC GGTGTCAGTG AAGCTCCGCA ACCGCGTGGT GCCGGGCCGC 540
GTGACCCAGA GCCAGGCCGA CTGGGACCGC GCTCGGCGCC GGCGCACCTT CTGCTTGCTG 600
GTGGTGGTCG TGGTGGTG 618
```

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 378  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE

(C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

```
GTGGTTCTGG TGCACCCGCT ACGTCGGCGC ATTTCACTGA GGCTCAGCGC CTACGCGGTG 60
CTGGGCATCT GGGCTCTATC TGCAGTGCTG GCGCTGCCGG CCGCGGTGCA CACCTACCAT 120
GTGGAGCTCA AGCCCCACGA CGTGAGCCTC TGCAGGAGT TCTGGGGCTC GCAGGAGCGC 180
CAACGCCAGA TCTACGCTG GGGGCTGCTT CTGGGCACCT ATTTGCTCCC CCTGCTGGCC 240
ATCCTCCTGT CTTACGTACG GGTGTCAGTG AAGTGAGGA ACCGCGTGGT GCCTGGCAGC 300
```



GTGACCCAGA GTCAAGCTGA CTGGGACCGA GCGCGTCGCC GCCGCACTTT CTGTCTGCTG 360  
 GTGGTGGTGG TGGTAGTG 378

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70  
 (B) TYPE: Amino acid  
 (C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Val	Cys	His	Val	Ile	Phe	Lys	Asn	Gln	Arg	Met	His	Ser	Ala	Thr	Ser
1			5					10						15	
Leu	Phe	Ile	Val	Asn	Leu	Ala	Val	Ala	Asp	Ile	Met	Ile	Thr	Leu	Ile
			20					25					30		
Asn	Thr	Pro	Phe	Thr	Leu	Val	Arg	Phe	Val	Asn	Ser	Thr	Trp	Ile	Phe
		35					40					45			
Gly	Lys	Gly	Met	Cys	His	Val	Ser	Arg	Phe	Ala	Gln	Tyr	Cys	Ser	Leu
	50					55					60				
His	Val	Ser	Ala	Leu	Thr										
65					70										

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71  
 (B) TYPE: Amino acid  
 (C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

Glu	Pro	Ala	Asp	Leu	Phe	Trp	Lys	Asn	Leu	Asp	Leu	Pro	Thr	Phe	Ile
1				5					10					15	
Leu	Leu	Asn	Ile	Leu	Pro	Leu	Leu	Ile	Ile	Ser	Val	Ala	Tyr	Val	Arg
			20					25					30		
Val	Thr	Lys	Lys	Leu	Trp	Leu	Cys	Asn	Met	Ile	Val	Asp	Val	Thr	Thr
		35					40					45			
Glu	Gln	Tyr	Phe	Ala	Leu	Arg	Pro	Lys	Lys	Lys	Lys	Thr	Ile	Lys	Met
	50					55						60			

Leu Met Leu Val Val Val Leu  
65 70

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 210  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE

(C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

GTCTGTCATG TCATCTTCAA GAACCAGCGA ATGCACTCGG CCACCAGCCT CTTCATCGTC 60  
AACCTGGCAG TTGCCGACAT AATGATCACG CTGCTCAACA CCCCTTCAC TTTGGTTCGC 120  
TTTGTGAACA GCACATGGAT ATTTGGGAAG GGCATGTGCC ATGTCAGCCG CTTTGCCCAG 180  
TACTGCTCAC TGCACGTCTC AGCACTGACA 210

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE

(C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

GAGCCAGCTG ACCTCTTCTG GAAGAACCTG GACTTGCCCA CCTTCATCCT GCTCAACATC 60  
CTGCCCCCTCC TCATCATCTC TGTGGCCTAC GTTCGTGTGA CCAAGAAACT GTGGCTGTGT 120  
AATATGATTG TCGATGTGAC CACAGAGCAG TACTTTGCCC TGCGGCCCAA AAAGAAGAAG 180  
ACCATCAAGA TGTGATGCT GGTGGTAGTC CTC 213

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115  
(B) TYPE: Amino acid  
(C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Ala Ser Trp His Lys Arg Gly Gly Arg Arg Ala Ala Trp Val Val Cys  
1 5 10 15  
Gly Val Val Trp Leu Ala Val Thr Ala Gln Cys Leu Pro Thr Ala Val  
20 25 30  
Phe Ala Ala Thr Gly Ile Gln Arg Asn Arg Thr Val Cys Tyr Asp Leu  
35 40 45  
Ser Pro Pro Ile Leu Ser Thr Arg Tyr Leu Pro Tyr Gly Met Ala Leu  
50 55 60  
Thr Val Ile Gly Phe Leu Leu Pro Phe Ile Ala Leu Leu Ala Cys Tyr  
65 70 75 80  
Cys Arg Met Ala Arg Arg Leu Cys Arg Gln Asp Gly Pro Ala Gly Pro  
85 90 95  
Val Ala Gln Glu Arg Arg Ser Lys Ala Ala Arg Met Ala Val Val Val  
100 105 110  
Ala Ala Val  
115

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 328  
(B) TYPE: Amino acid  
(C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

Met Glu Gln Asp Asn Gly Thr Ile Gln Ala Pro Gly Leu Pro Pro Thr  
1 5 10 15  
Thr Cys Val Tyr Arg Glu Asp Phe Lys Arg Leu Leu Leu Thr Pro Val  
20 25 30  
Tyr Ser Val Val Leu Val Val Gly Leu Pro Leu Asn Ile Cys Val Ile  
35 40 45

Ala	Gln	Ile	Cys	Ala	Ser	Arg	Arg	Thr	Leu	Thr	Arg	Ser	Ala	Val	Tyr	50	55	60
Thr	Leu	Asn	Leu	Ala	Leu	Ala	Asp	Leu	Met	Tyr	Ala	Cys	Ser	Leu	Pro	65	70	75
Leu	Leu	Ile	Tyr	Asn	Tyr	Ala	Arg	Gly	Asp	His	Trp	Pro	Phe	Gly	Asp	85	90	95
Leu	Ala	Cys	Arg	Phe	Val	Arg	Phe	Leu	Phe	Tyr	Ala	Asn	Leu	His	Gly	100	105	110
Ser	Ile	Leu	Phe	Leu	Thr	Cys	Ile	Ser	Phe	Gln	Arg	Tyr	Leu	Gly	Ile	115	120	125
Cys	His	Pro	Leu	Ala	Ser	Trp	His	Lys	Arg	Gly	Gly	Arg	Arg	Ala	Ala	130	135	140
Trp	Val	Val	Cys	Gly	Val	Val	Trp	Leu	Ala	Val	Thr	Ala	Gln	Cys	Leu	145	150	155
Pro	Thr	Ala	Val	Phe	Ala	Ala	Thr	Gly	Ile	Gln	Arg	Asn	Arg	Thr	Val	165	170	175
Cys	Tyr	Asp	Leu	Ser	Pro	Pro	Ile	Leu	Ser	Thr	Arg	Tyr	Leu	Pro	Tyr	180	185	190
Gly	Met	Ala	Leu	Thr	Val	Ile	Gly	Phe	Leu	Leu	Pro	Phe	Ile	Ala	Leu	195	200	205
Leu	Ala	Cys	Tyr	Cys	Arg	Met	Ala	Arg	Arg	Leu	Cys	Arg	Gln	Asp	Gly	210	215	220
Pro	Ala	Gly	Pro	Val	Ala	Gln	Glu	Arg	Arg	Ser	Lys	Ala	Ala	Arg	Met	225	230	235
Ala	Val	Val	Val	Ala	Ala	Val	Phe	Ala	Ile	Ser	Phe	Leu	Pro	Phe	His	245	250	255
Ile	Thr	Lys	Thr	Ala	Tyr	Leu	Ala	Val	Arg	Ser	Thr	Pro	Gly	Val	Ser	260	265	270
Cys	Pro	Val	Leu	Glu	Thr	Phe	Ala	Ala	Ala	Tyr	Lys	Gly	Thr	Arg	Pro	275	280	285
Phe	Ala	Ser	Val	Asn	Ser	Val	Leu	Asp	Pro	Ile	Leu	Phe	Tyr	Phe	Thr	290	295	300
Gln	Gln	Lys	Phe	Arg	Arg	Gln	Pro	His	Asp	Leu	Leu	Gln	Arg	Leu	Thr	305	310	315
Ala	Lys	Trp	Gln	Arg	Gln	Arg	Val									325		

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 345  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE  
(C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

GCTTCCTGGC ACAAGCGTGG AGGTCGCCGT GCTGCTTGGG TAGTGTGTGG AGTCGTGTGG 60  
CTGGCTGTGA CAGCCCAGTG CCTGCCCACG GCAGTCTTTG CTGCCACAGG CATCCAGCGC 120  
AACCGCACTG TGTGCTACGA CCTGAGCCCA CCCATCCTGT CTACTCGCTA CCTGCCCTAT 180  
GGTATGGCCC TCACGGTCAT CGGCTTCTTG CTGCCCTTCA TAGCCTTACT GGCTTGTTAT 240  
TGTCGCATGG CCCGCCGCCT GTGTCGCCAG GATGGCCCAG CAGGTCCTGT GGCCAAGAG 300  
CGGCGCAGCA AGGCGGCTCG TATGGCTGTG GTGGTGGCAG CTGTC  
SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Shuji Hinuma  
Masaki Hosoya  
Ryo Fujii  
Tetsuya Ohtaki  
Shoji Fukusumi

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Shuji Hinuma  
Masaki Hosoya  
Ryo Fujii  
Tetsuya Ohtaki  
Shoji Fukusumi

T CGGTGGTGCT GGTGGTCGGC 120  
CTGCCACTGA ACATCTGCGT CATTGCCCAG ATCTGCGCAT CCCGCCGGAC CCTGACCCGT 180  
TCCGCTGTGT ACACCCTGAA CCTGGCACTG GCGGACCTGA TGTATGCCTG TTCACTACCC 240  
CTACTTATCT ATAACTACGC CAGAGGGGAC CACTGGCCCT TCGGAGACCT CGCCTGCCGC 300  
TTTGTACGCT TCCTCTTCTA TGCCAATCTA CATGGCAGCA TCCTGTTCTT CACCTGCATT 360  
AGCTTCCAGC GCTACCTGGG CATCTGCCAC CCCCTGGCTT CCTGGCACAA GCGTGGAGGT 420

CGCCGTGCTG CTTGGGTAGT GTGTGGAGTC GTGTGGCTGG CTGTGACAGC CCAGTGCCTG 480  
 CCCACGGCAG TCTTTGCTGC CACAGGCATC CAGCGCAACC GCACTGTGTG CTACGACCTG 540  
 AGCCCACCCA TCCTGTCTAC TCGCTACCTG CCCTATGGTA TGGCCCTCAC GGTCATCGGC 600  
 TTCTTGCTGC CCTTCATAGC CTTACTGGCT TGTTATTGTC GCATGGCCCG CCGCCTGTGT 660  
 CGCCAGGATG GCCCAGCAGG TCCTGTGGCC CAAGAGCGGC GCAGCAAGGC GGCTCGTATG 720  
 GCTGTGGTGG TGGCAGCTGT CTTTGCCATC AGCTTCCTGC CTTTCCACAT CACCAAGACA 780  
 GCCTACTTGG CTGTGCGCTC CACGCCCGGT GTCTCTTGCC CTGTGCTGGA GACCTTCGCT 840  
 GCTGCCTACA AAGGCACTCG GCCCTTCGCC AGTGTCACA GTGTTCTGGA CCCATTCTC 900  
 TTCTACTTCA CACAACAGAA GTTCCGGCGG CAACCCACG ATCTCTTACA GAGGCTCACA 960  
 GCCAAGTGGC AGAGGCAGAG AGTC 984

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128  
 (B) TYPE: Amino acid  
 (C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

Ala	Ala	Met	Ser	Val	Asp	Arg	Tyr	Val	Ala	Ile	Val	His	Ser	Arg	Arg	1	5	10	15
Ser	Ser	Ser	Leu	Arg	Val	Ser	Arg	Asn	Ala	Leu	Leu	Gly	Val	Gly	Phe	20	25	30	
Ile	Trp	Ala	Leu	Ser	Ile	Ala	Met	Ala	Ser	Pro	Val	Ala	Tyr	His	Gln	35	40	45	
Arg	Leu	Phe	His	Arg	Asp	Ser	Asn	Gln	Thr	Phe	Cys	Trp	Glu	Gln	Trp	50	55	60	
Pro	Asn	Lys	Leu	His	Lys	Lys	Ala	Tyr	Val	Val	Cys	Thr	Phe	Val	Phe	65	70	75	80
Gly	Tyr	Leu	Leu	Pro	Leu	Leu	Leu	Ile	Cys	Phe	Cys	Tyr	Ala	Lys	Val	85	90	95	
Leu	Asn	His	Leu	His	Lys	Lys	Leu	Lys	Asn	Met	Ser	Lys	Lys	Ser	Glu	100	105	110	
Ala	Ser	Lys	Lys	Lys	Thr	Ala	Gln	Thr	Val	Leu	Val	Val	Val	Val	Val	115	120	125	

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 384  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE

(C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

```
GCCGCGATGT CTGTGGATCG CTACGTGGCC ATTTGTGCACT CGCGGCGCTC CTCCTCCCTC      60
AGGGTGTCCC GCAACGCACT GCTGGGCGTG GGCTTCATCT GGGCGCTGTC CATCGCCATG      120
GCCTCGCCGG TGGCCTACCA CCAGCGTCTT TTCCATCGGG ACAGCAACCA GACCTTCTGC      180
TGGGAGCAGT GGCCCAACAA GCTCCACAAG AAGGCTTACG TGGTGTGCAC TTTCGTCTTT      240
GGGTACCTTC TGCCCTTACT GTCATCTGC TTTTGCTATG CCAAGGTCCT TAATCATCTG      300
CATAAAAAGC TGAAAAACAT GTCAAAAAAG TCTGAAGCAT CCAAGAAAAA GACTGCACAG      360
ACCGTCCTGG TGGTCGTTGT AGTA                                           384
```

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71  
(B) TYPE: Amino acid  
(C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

```
Val Leu Trp Phe Phe Gly Phe Ser Ile Lys Arg Thr Pro Phe Ser Val
 1              5              10              15
Tyr Phe Leu His Leu Ala Ser Ala Asp Gly Ala Tyr Leu Phe Ser Lys
                20              25              30
Ala Val Phe Ser Leu Leu Asn Ala Gly Gly Phe Leu Gly Thr Phe Ala
                35              40              45
His Tyr Val Arg Ser Val Ala Arg Val Leu Gly Leu Cys Ala Phe Val
 50              55              60
Ala Gly Val Ser Leu Leu Pro
```

## (2) INFORMATION FOR SEQ ID NO: 45:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 215  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

## (ix) FEATURE

(C) IDENTIFICATION METHOD: S

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

```

GTGCTCTGGT TCTTCGGCTT CTCCATCAAG AGGACCCCCT TCTCCGTCTA CTCCTGCAC      60
CTGGCCAGCG CCGACGGCGC CTACCTCTTC AGCAAGGCCG TGTCTCCCT GCTGAACGCC      120
GGCGGCTTCC TGGGCACCTT CGCCCACTAT GTGCGCAGCG TGGCCCGGGT GCTGGGGCTC      180
TGCGCCTTCG TGGCGGGCGT GAGCCTCCTG CCGGC                                215

```

## (2) INFORMATION FOR SEQ ID NO: 46:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 348  
 (B) TYPE: Amino acid  
 (C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

```

Met Glu Leu Ala Met Val Asn Leu Ser Glu Gly Asn Gly Ser Asp Pro
 1             5             10             15
Glu Pro Pro Ala Pro Glu Ser Arg Pro Leu Phe Gly Ile Gly Val Glu
      20             25             30
Asn Phe Ile Thr Leu Val Val Phe Gly Leu Ile Phe Ala Met Gly Val
      35             40             45
Leu Gly Asn Ser Leu Val Ile Thr Val Leu Ala Arg Ser Lys Pro Gly
      50             55             60
Lys Pro Arg Ser Thr Thr Asn Leu Phe Ile Leu Asn Leu Ser Ile Ala
      65             70             75             80
Asp Leu Ala Tyr Leu Leu Phe Cys Ile Pro Phe Gln Ala Thr Val Tyr
      85             90             95
Ala Leu Pro Thr Trp Val Leu Gly Ala Phe Ile Cys Lys Phe Ile His
      100            105            110

```



Tyr	Phe	Phe	Thr	Val	Ser	Met	Leu	Val	Ser	Ile	Phe	Thr	Leu	Ala	Ala			
		115					120					125						
Met	Ser	Val	Asp	Arg	Tyr	Val	Ala	Ile	Val	His	Ser	Arg	Arg	Ser	Ser			
	130					135					140							
Ser	Leu	Arg	Val	Ser	Arg	Asn	Ala	Leu	Leu	Gly	Val	Gly	Phe	Ile	Trp			
145					150					155					160			
Ala	Leu	Ser	Ile	Ala	Met	Ala	Ser	Pro	Val	Ala	Tyr	His	Gln	Arg	Leu			
				165					170					175				
Phe	His	Arg	Asp	Ser	Asn	Gln	Thr	Phe	Cys	Trp	Glu	Gln	Trp	Pro	Asn			
			180					185					190					
Lys	Leu	His	Lys	Lys	Ala	Tyr	Val	Val	Cys	Thr	Phe	Val	Phe	Gly	Tyr			
		195					200						205					
Leu	Leu	Pro	Leu	Leu	Leu	Ile	Cys	Phe	Cys	Tyr	Ala	Lys	Val	Leu	Asn			
	210					215					220							
His	Leu	His	Lys	Lys	Leu	Lys	Asn	Met	Ser	Lys	Lys	Ser	Glu	Ala	Ser			
225					230					235					240			
Lys	Lys	Lys	Thr	Ala	Gln	Thr	Val	Leu	Val	Val	Val	Val	Val	Phe	Gly			
			245						250					255				
Ile	Ser	Trp	Leu	Pro	His	His	Val	Val	His	Leu	Trp	Ala	Glu	Phe	Gly			
		260					265						270					
Ala	Phe	Pro	Leu	Thr	Pro	Ala	Ser	Phe	Phe	Phe	Arg	Ile	Thr	Ala	His			
		275					280					285						
Cys	Leu	Ala	Tyr	Ser	Asn	Ser	Ser	Val	Asn	Pro	Ile	Ile	Tyr	Ala	Phe			
	290					295					300							
Leu	Ser	Glu	Asn	Phe	Arg	Lys	Ala	Tyr	Lys	Gln	Val	Phe	Lys	Cys	His			
305					310					315					320			
Val	Cys	Asp	Glu	Ser	Pro	Arg	Ser	Glu	Thr	Lys	Glu	Asn	Lys	Ser	Arg			
			325					330						335				
Met	Asp	Thr	Pro	Pro	Ser	Thr	Asn	Cys	Thr	His	Val							
			340					345										

(2) INFORMATION FOR SEQ ID NO: 47:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1044
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Double
  - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: cDNA

(ix) FEATURE

(C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

ATGGA	ACTGG	CTATG	GTGAA	CCTCA	GTGAA	GGGA	AATGG	GGA	GCGA	CCCAG	A	GCCG	CCAG	CC	60
CCGG	AGTCC	AGGCC	GTCTT	CGGC	ATTGG	C	GTGG	AGAA	CT	TCAT	TACG	CT	GGTA	GTGT	120
GGCCT	GATTT	TCGCG	ATGGG	CGTG	CTGGG	C	AACAG	CCTGG	TGAT	CACCG	T	GCTG	GC	CGC	180
AGCAA	ACCAG	GCAAC	CCCCG	CAGCA	CCACC	A	ACCTG	TTTA	TCCT	CAAT	CT	GAGCA	TC	GCA	240
GACCT	GGCCT	ACCTG	CTCTT	CTGCA	TCCCT	T	TTTCA	GGCCA	CCGT	GTAT	GC	ACTG	CCC	ACC	300
TGGGT	GCTGG	GCGCT	TCAT	CTGCA	AGTTT	A	ATACT	ACT	TCTT	CACCG	T	GTCC	ATG	CTG	360
GTGAG	CATCT	TCACC	CTGGC	CGCG	ATGTCT	G	GTGG	ATCG	CT	ACGT	GGCC	AT	TGTG	CACTCG	420
CGGCG	CTCCT	CCTCC	CTCAG	GGTG	TCCCG	C	AACGC	ACTGC	TGGG	CGTGG	G	CTTCA	TCT	GG	480
GCGCT	GTCCA	TCGCC	ATGGC	CTCG	CCGGT	G	GCCTA	CCACC	AGCG	TCTTTT	CCAT	CGGG	A	C	540
AGCAA	CCAGA	CCTTCT	GCTG	GGAG	CAGTGG	C	CCCA	ACAAGC	TCC	ACAAG	AA	GGCT	TAC	GTG	600
GTGTG	CACTT	TCGTCT	TTGG	GTAC	CTTCTG	C	CCCT	TACTGC	TCAT	CTGCTT	TTG	CTAT	G	CC	660
AAGGT	CCTTA	ATCAT	CTGCA	TAAAA	AAGCTG	A	AAAA	CATGT	CAAAA	AAGTC	TGA	AGCA	TCC		720
AAGAAA	AAGA	CTGC	ACAGAC	CGTC	CTGGT	G	GTCG	TGTAG	TATTT	TGGCAT	ATC	CTGG	CTG		780
CCCC	ATCATG	TCGT	CCACCT	CTGGG	CTGAG	T	TTGG	AGCCT	TCCC	ACTGAC	GCC	AGCT	TCC		840
TTCTT	CTTTCA	GAAT	CACCGC	CCATT	GCCTG	G	GCATA	CAGCA	ACTC	CTCAGT	GA	ACCC	CATC		900
ATAT	ATGCCT	TTCT	CTCAGA	AAACT	TCCGG	A	AAGG	CGTACA	AGCA	AGTGTT	CA	AGTG	TCAT		960
GTTT	GCGATG	AATCT	CCACG	CAGT	GAAACT	A	AAGG	AAAACA	AGAG	CCGGAT	GGAC	ACCC	CG		1020
CCAT	CCACCA	ACTG	CACCCA	CGTG											1044

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125  
(B) TYPE: Amino acid  
(C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

Leu	Leu	Thr	Leu	His	Pro	Val	Trp	Ser	Gln	Lys	His	Arg	Thr	Ser	His
1				5					10					15	

Trp Ala Ser Arg Val Val Leu Gly Val Trp Leu Ser Ala Thr Ala Phe  
                     20                    25                    30  
 Ser Val Pro Tyr Leu Val Phe Arg Glu Thr Tyr Asp Asp Arg Lys Gly  
                     35                    40                    45  
 Arg Val Thr Cys Arg Asn Asn Tyr Ala Val Ser Thr Asp Trp Glu Ser  
                     50                    55                    60  
 Lys Glu Met Gln Thr Val Arg Gln Trp Ile His Ala Thr Cys Phe Ile  
                     65                    70                    75                    80  
 Ser Arg Phe Ile Leu Gly Phe Leu Leu Pro Phe Leu Val Ile Gly Phe  
                     85                    90                    95  
 Cys Tyr Glu Arg Val Ala Arg Lys Met Lys Glu Arg Gly Leu Phe Lys  
                     100                    105                    110  
 Ser Ser Lys Pro Phe Lys Val Thr Met Thr Ala Val Ile  
                     115                    120                    125

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:  
     (A) LENGTH: 377  
     (B) TYPE: Nucleic acid  
     (C) STRANDEDNESS: Double  
     (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE  
     (C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

CTTCTCACCC TTCACCCAGT GTGGTCCCAA AAGCACCGAA CCTCACACTG GGCTTCCAGA	60
GTCGTTCTGG GAGTCTGGCT CTCTGCCACT GCCTTCAGCG TGCCCTATTT GGTTTTCAGG	120
GAGACATATG ATGACCGTAA AGGAAGAGTG ACCTGCAGAA ATAACCTACGC TGTGTCCACT	180
GACTGGGAAA GCAAAGAGAT GCAAACAGTA AGACAATGGA TTCATGCCAC CTGTTTCATC	240
AGCCGCTTCA TACTGGGCTT CCTTCTGCCT TTCTTAGTCA TTGGCTTTTG TTATGAAAGA	300
GTAGCCCGCA AGATGAAAGA GAGGGGCCTC TTAAATCCA GCAAACCCTT CAAAGTCACG	360
ATGACTGCTG TTATCTC	377

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 119  
(B) TYPE: Amino acid  
(C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Phe Lys Ile Val Lys Pro Leu Ser Thr Ser Phe Ile Gln Ser Val Asn  
1 5 10 15  
Tyr Ser Lys Leu Val Ser Leu Val Val Trp Leu Leu Met Leu Leu Leu  
20 25 30  
Ala Val Pro Asn Val Ile Leu Thr Asn Gln Arg Val Lys Asp Val Thr  
35 40 45  
Gln Ile Lys Cys Met Glu Leu Lys Asn Glu Leu Gly Arg Gln Trp His  
50 55 60  
Lys Ala Ser Asn Tyr Ile Phe Val Gly Ile Phe Trp Leu Val Phe Leu  
65 70 75 80  
Leu Leu Ile Ile Phe Tyr Thr Ala Ile Thr Arg Lys Ile Phe Lys Ser  
85 90 95  
His Leu Lys Ser Arg Lys Asn Ser Ile Ser Val Lys Lys Lys Ser Ser  
100 105 110  
Arg Asn Ile Phe Ser Ile Val  
115

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 357  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE

(C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

TTCAAGATTG TGAAGCCCCT TTCCACGTCC TTCATCCAGT CTGTGAACTA CAGCAAATC 60  
GTCTCGCTGG TGGTCTGGTT GCTCATGCTC CTCCTCGCCG TCCCCAACGT CATTCTCACC 120  
AACCAGAGAG TTAAGGACGT GACGCAGATA AAATGCATGG AACTTAAAAA CGAACTGGGC 180  
CGCCAGTGGC ACAAGGCGTC AAATAACATC TTTGTGGGCA TTTTCTGGCT TGTGTTCTT 240

TTGCTAATCA TTTTCTACAC TGCTATCACC AGGAAAATCT TTAAGTCCCA CCTGAAATCC 300  
 AGAAAGAATT CCATCTCGGT CAAAAAGAAA TCTAGCCGCA ACATCTTCAG CATCGTG 357

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 252  
 (B) TYPE: Amino acid  
 (C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

Val	Asp	Leu	Leu	Ala	Ala	Leu	Thr	Leu	Met	Pro	Leu	Ala	Met	Leu	Ser	1	5	10	15
Ser	Ser	Ala	Leu	Phe	Asp	His	Ala	Leu	Phe	Gly	Glu	Val	Ala	Cys	Arg	20	25	30	
Leu	Tyr	Leu	Phe	Leu	Ser	Val	Cys	Phe	Val	Ser	Leu	Ala	Ile	Leu	Ser	35	40	45	
Val	Ser	Ala	Ile	Asn	Val	Glu	Arg	Tyr	Tyr	Tyr	Val	Val	His	Pro	Met	50	55	60	
Arg	Tyr	Glu	Val	Arg	Met	Lys	Leu	Gly	Leu	Val	Ala	Ser	Val	Leu	Val	65	70	75	80
Gly	Val	Trp	Val	Lys	Ala	Leu	Ala	Met	Ala	Ser	Val	Pro	Val	Leu	Gly	85	90	95	
Arg	Val	Ser	Trp	Glu	Glu	Gly	Pro	Pro	Ser	Val	Pro	Pro	Gly	Cys	Ser	100	105	110	
Leu	Gln	Trp	Ser	His	Ser	Ala	Tyr	Cys	Gln	Leu	Phe	Val	Val	Val	Phe	115	120	125	
Ala	Val	Leu	Tyr	Phe	Leu	Leu	Pro	Leu	Leu	Leu	Ile	Leu	Val	Val	Tyr	130	135	140	
Cys	Ser	Met	Phe	Arg	Val	Ala	Arg	Val	Ala	Ala	Met	Gln	His	Gly	Pro	145	150	155	160
Leu	Pro	Thr	Trp	Met	Glu	Thr	Pro	Arg	Gln	Arg	Ser	Glu	Ser	Leu	Ser	165	170	175	
Ser	Arg	Ser	Thr	Met	Val	Thr	Ser	Ser	Gly	Ala	Pro	Gln	Thr	Thr	Pro	180	185	190	
His	Arg	Thr	Phe	Gly	Gly	Gly	Lys	Ala	Ala	Val	Val	Leu	Leu	Ala	Val	195	200	205	

Gly Gly Gln Phe Leu Leu Cys Trp Leu Pro Tyr Phe Ser Phe His Leu  
 210 215 220

Tyr Val Ala Leu Ser Ala Gln Pro Ile Ala Ala Gly Gln Val Glu Asn  
 225 230 235 240

Val Val Thr Trp Ile Gly Tyr Phe Cys Phe Thr Ser  
 245 250

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 756  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE

(C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

GTGGACCTGC TGGCTGCCCT GACCCTCATG CCTCTGGCCA TGCTCTCCAG CTCCGCCCTC 60  
 TTTGACCACG CCCTCTTTGG GGAGGTGGCC TGCCGCCTCT ACTTGTTCTT GAGCGTCTGC 120  
 TTTGTCAGCC TGGCCATCCT CTCGGTGTCC GCCATCAATG TGGAGCGCTA CTATTATGTG 180  
 GTCCACCCCA TGCCTATGA GGTGCGCATG AACTGGGGC TGGTGGCCTC TGTGCTGGTG 240  
 GCGGTGTGGG TGAAGGCCCT GGCCATGGCT TCTGTGCCAG TGTTGGGAAG GGTGTCCTGG 300  
 GAGGAAGGCC CTCCAGTGT CCCCCAGGC TGTTCCTCC AATGGAGCCA CAGTGCCTAC 360  
 TGCCAGCTTT TCGTGGTGGT CTTGCGCGTC CTCTACTTCC TGCTGCCCCCT GTCCTCATC 420  
 CTTGTGGTCT ACTGCAGCAT GTTCCGGGTG GCTCGTGTGG CTGCCATGCA GCACGGGCCG 480  
 CTGCCCACGT GGATGGAGAC GCCCCGGCAA CGCTCCGAGT CTCTCAGCAG CCGCTCCACT 540  
 ATGGTCACCA GCTCGGGGGC CCCGAGACC ACCCCTCACC GGACGTTTGG CGGAGGGAAG 600  
 GCAGCAGTGG TCCTCCTGGC TGTGGGAGGA CAGTTCCTGC TCTGTTGGTT GCCCTACTTC 660  
 TCCTTCCACC TCTATGTGGC CCTGAGCGCT CAGCCCATTG CAGCGGGGCA GGTGGAGAAC 720  
 GTGGTGACCT GGATTGGCTA CTTCTGCTTC ACCTCC 756

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:



## (2) INFORMATION FOR SEQ ID NO: 55:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 789  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

## (ix) FEATURE

(C) IDENTIFICATION METHOD: S

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

```

GCCGATGTGC TGGTGACAGC CATCTGCCTG CCGGCCAGTC TGCTGGTAGA CATCACGGAA    60
TCCTGGCTCT TTGGCCATGC CCTCTGCAAG GTCATCCCCT ATCTACAGGC CGTGTCCTGTG    120
TCAGTGGTCG TGCTGACTCT CAGCTCCATC GCCCTGGACC GCTGGTACGC CATCTGCCAC    180
CCGCTGTTGT TCAAGAGCAC TGCCCGGCGC GCCCGCGGCT CCATCCTCGG CATCTGGGCG    240
GTGTCGCTGG CTGTCATGGT GCCTCAGGCT GCTGTCATGG AGTGTAGCAG CGTGCTGCCC    300
GAGCTGGCCA ACCGCACCCG CCTCCTGTCT GTCTGTGATG AGCGCTGGGC AGACGACCTG    360
TACCCCAAGA TCTACCACAG CTGCTTCTTC ATTGTCACCT ACCTGGCCCC ACTGGGCCTC    420
ATGGCCATGG CCTATTTCCA GATCTTCCGC AAGCTCTGGG GCCGCCAGAT CCCCGGCACC    480
ACCTCGGCCC TGGTGCGCAA CTGGAAGCGG CCCTCAGACC AGCTGGACGA CCAGGGCCAG    540
GGCCTGAGCT CAGAGCCCCA GCCCCGGGCC CGCGCCTTCC TGGCCGAGGT GAAACAGATG    600
CGAGCCCGGA GGAAGACGGC CAAGATGCTG ATGGTGGTGC TGCTGGTCTT CGCCCTCTGC    660
TACCTGCCCA TCAGTGTCTT CAACGTCCTC AAGAGGGTCT TCGGGATGTT CCGCCAAGCC    720
AGCGACCGAG AGGCCATCTA CGCCTGCTTC ACCTTCTCCC ACTGGCTGGT GTACGCCAAC    780
AGCGCCGCC                                     789
  
```

## (2) INFORMATION FOR SEQ ID NO: 56:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 328  
 (B) TYPE: Amino acid  
 (C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

Met	Glu	Trp	Asp	Asn	Gly	Thr	Gly	Gln	Ala	Leu	Gly	Leu	Pro	Pro	Thr	
1				5					10						15	
Thr	Cys	Val	Tyr	Arg	Glu	Asn	Phe	Lys	Gln	Leu	Leu	Leu	Pro	Pro	Val	
			20					25					30			
Tyr	Ser	Ala	Val	Leu	Ala	Ala	Gly	Leu	Pro	Leu	Asn	Ile	Cys	Val	Ile	
		35					40					45				
Thr	Gln	Ile	Cys	Thr	Ser	Arg	Arg	Ala	Leu	Thr	Arg	Thr	Ala	Val	Tyr	
	50					55					60					
Thr	Leu	Asn	Leu	Ala	Leu	Ala	Asp	Leu	Leu	Tyr	Ala	Cys	Ser	Leu	Pro	
65					70					75					80	
Leu	Leu	Ile	Tyr	Asn	Tyr	Ala	Gln	Gly	Asp	His	Trp	Pro	Phe	Gly	Asp	
				85					90					95		
Phe	Ala	Cys	Arg	Leu	Val	Arg	Phe	Leu	Phe	Tyr	Ala	Asn	Leu	His	Gly	
			100					105					110			
Ser	Ile	Leu	Phe	Leu	Thr	Cys	Ile	Ser	Phe	Gln	Arg	Tyr	Leu	Gly	Ile	
		115					120					125				
Cys	His	Pro	Leu	Ala	Pro	Trp	His	Lys	Arg	Gly	Gly	Arg	Arg	Ala	Ala	
	130					135					140					
Trp	Leu	Val	Cys	Val	Thr	Val	Trp	Leu	Ala	Val	Thr	Thr	Gln	Cys	Leu	
145					150					155					160	
Pro	Thr	Ala	Ile	Phe	Ala	Ala	Thr	Gly	Ile	Gln	Arg	Asn	Arg	Thr	Val	
			165					170						175		
Cys	Tyr	Asp	Leu	Ser	Pro	Pro	Ala	Leu	Ala	Thr	His	Tyr	Met	Pro	Tyr	
		180						185					190			
Gly	Met	Ala	Leu	Thr	Val	Ile	Gly	Phe	Leu	Leu	Pro	Phe	Ala	Ala	Leu	
	195						200					205				
Leu	Ala	Cys	Tyr	Cys	Leu	Leu	Ala	Cys	Arg	Leu	Cys	Arg	Gln	Asp	Gly	
	210					215					220					
Pro	Ala	Glu	Pro	Val	Ala	Gln	Glu	Arg	Arg	Gly	Lys	Ala	Ala	Arg	Met	
225				230						235					240	
Ala	Val	Val	Val	Ala	Ala	Ala	Phe	Ala	Ile	Ser	Phe	Leu	Pro	Phe	His	
				245				250						255		
Ile	Thr	Lys	Thr	Ala	Tyr	Leu	Ala	Val	Gly	Ser	Thr	Pro	Gly	Val	Pro	
		260						265					270			
Cys	Thr	Val	Leu	Glu	Ala	Phe	Ala	Ala	Ala	Tyr	Lys	Gly	Thr	Arg	Pro	
	275					280						285				

Phe Ala Ser Ala Asn Ser Val Leu Asp Pro Ile Leu Phe Tyr Phe Thr  
 290 295 300

Gln Lys Lys Phe Arg Arg Arg Pro His Glu Leu Leu Gln Lys Leu Thr  
 305 310 315 320

Ala Lys Trp Gln Arg Gln Gly Arg  
 325

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 984  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE  
 (C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

ATGGAATGGG ACAATGGCAC AGGCCAGGCT CTGGGCTTGC CACCCACCAC CTGTGTCTAC	60
CGCGAGAACT TCAAGCAACT GCTGCTGCCA CCTGTGTATT CGGCGGTGCT GGCGGCTGGC	120
CTGCCGCTGA ACATCTGTGT CATTACCCAG ATCTGCACGT CCCGCCGGGC CCTGACCCGC	180
ACGGCCGTGT ACACCCTAAA CCTTGCTCTG GCTGACCTGC TATATGCCTG CTCCCTGCCC	240
CTGCTCATCT ACAACTATGC CCAAGGTGAT CACTGGCCCT TTGGCGACTT CGCCTGCCGC	300
CTGGTCCGCT TCCTCTTCTA TGCCAACCTG CACGGCAGCA TCCTCTTCCT CACCTGCATC	360
AGCTTCCAGC GCTACCTGGG CATCTGCCAC CCGCTGGCCC CCTGGCACAA ACGTGGGGGC	420
CGCCGGGCTG CCTGGCTAGT GTGTGTAACC GTGTGGCTGG CCGTGACAAC CCAGTGCCTG	480
CCCACAGCCA TCTTCGCTGC CACAGGCATC CAGCGTAACC GCACTGTCTG CTATGACCTC	540
AGCCCGCCTG CCCTGGCCAC CCACTATATG CCCTATGGCA TGGCTCTCAC TGTCATCGGC	600
TTCTTGCTGC CCTTTGCTGC CCTGCTGGCC TGCTACTGTC TCCTGGCCTG CCGCCTGTGC	660
CGCCAGGATG GCCCGGCAGA GCCTGTGGCC CAGGAGCGGC GTGGCAAGGC GGCCCGCATG	720
GCCGTGGTGG TGGCTGCTGC CTTTGCCATC AGCTTCCTGC CTTTTCACAT CACCAAGACA	780
GCCTACCTGG CAGTGGGCTC GACGCCGGGC GTCCCCTGCA CTGTATTGGA GGCCTTTGCA	840
GCGGCCTACA AAGGCACGCG GCCGTTTGCC AGTGCCAACA GCGTGCTGGA CCCCATCCTC	900
TTCTACTTCA CCCAGAAGAA GTTCCGCCGG CGACCACATG AGCTCCTACA GAAACTCACA	960

## (2) INFORMATION FOR SEQ ID NO: 58:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid  
Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

ACAGCCATCT TCGTGCCAC AGGCAT 26

## (2) INFORMATION FOR SEQ ID NO: 59:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid  
Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

AGACAGTAGC AGGCCAGCAG GGCAGCAA 29

## (2) INFORMATION FOR SEQ ID NO: 60:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid  
Synthetic DNA

(iii) FEATURES: N is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

CTGTGYGYSA TYGCNNTKGA YMGSTAC 27

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid  
Synthetic DNA

(iii) FEATURES: N is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

AKGWAGWAGG GCAGCCAGCA GANSRYGAA

29

□

Cont  
Dr